

SEQ ID NO: 12 (searched SEQ ID NO: 11, has mismatch therefore SEQ ID NO: 11).

RESULT 11

HSU70323

LOCUS HSU70323 4481 bp mRNA PRI 20-NOV-1996

DEFINITION Human ataxin-2 (SCA2) mRNA, complete cds.

ACCESSION U70323

VERSION U70323.1 GI:1679683

KEYWORDS .

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4481)

AUTHORS Pulst,S.-M., Nechiporuk,A., Nechiporuk,T., Gispert,S., Chen,X.-N., Lopes-Cendes,I., Pearlman,S., Starkman,S., Orozco-Diaz,G., Lunkes,A., DeJong,P., Rouleau,G.A., Auburger,G., Korenberg,J.R., Figueroa,C. and Sahba,S.

TITLE Moderate expansion of a normally biallelic trinucleotide repeat in

spinocerebellar ataxia type 2
JOURNAL Nature Genet. 14 (3), 269-276 (1996)

MEDLINE 97051920

REFERENCE 2 (bases 1 to 4481)

AUTHORS Pulst,S.-M.

TITLE Direct Submission

JOURNAL Submitted (10-SEP-1996) Medicine, Cedars-Sinai, 8700 Beverly Blvd., Los Angeles, CA 90048, USA

FEATURES Location/Qualifiers

source 1. .4481
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
/map="12q24.1"

gene 163. .4101
/gene="SCA2"

CDS 163. .4101
/gene="SCA2"
/standard_name="spinocerebellar ataxia type 2"
/codon_start=1
/product="ataxin-2"
/protein_id="AAB19200.1"
/db_xref="GI:1679684"

/translation="MRSAAAAPRSPAVATESRRFAAARWPGWRS LQRPARRSGRGGGG

AAPGPYP SAAPPPPGPGPPPSRQSSPPSASDCFGSNGNGGGA FRPGSRRL LGLGGPPR

PFVVVLLPLASPGAPPAAPTRASPLGARASPPRSGVSLARPAPGCPRP ACEPVYGPLT

```

MSLKPQQQQQQQQQQQQQQQQQQQQPPPAANVRKPGGSGLLASPAAAPSPSSSSV
SSSSATAPSSVVAATSGGGRPGLGRGRNSNKGLPQSTISFDGIYANMRMVHILTSVVG
SKCEVQVKNGGIYEGVFKTYSKCDLVLDAAHEKSTESSSGPKREEIMESILFKCSDF
VVVQFKDMDSSYAKRDAFTDSAISAKVNGEHKEKDLEPWDAGELTANEELEALENDVS
NGWDPNDMFRYNEENYGVVSTYDSSLSSYTVPLERDNSEEFKREARANQLAEEIESS
AQYKARVALENDDRSEEEKYTAVQRNSSEREGHSINTRENKYIPPGQRNREVISWGS
RQNSPRMGQPGSGSMPSRSTSHTSDFNPNSGSDQRVVNGGVPWPSPCPSPPSRPPSRY
QSGPNLPPRAATPTRPPSRPPSRPPSHPSAHGSPAPVSTMPKRMSSEGPPRMS
KAQRHPRNHRVSAGRGSISSGLEFVSHNPPSEAATPPVARTSPSGGTWSSVVGVPRL
SPKTHRPRSPRQNSIGNTPSGPVLASQAGIIPTEAVAMPIPAASPTPASPNRAVT
PSSEAKDSRLQDQRQNSPAGNKENIKPNETSPSFKAENKGISPVVSEHRKQIDDLKK
FKNDFRLQPSSTSESMDQLLNKNREGEKSRDLIKDIEPSAKDSFIENSSSNCTSGSS
KPNSPSISPSILSNTEHKGPEVTSQGVQTSSPACKQEKDDKEEKKDAAEQVRKSTLN
PNAKEFNPRSFSPQPKSTTPTSPRPQAQPSPMVGHQQPTPVYTQPVCFAPNMMYPVP
VSPGVQPLYPIPMTPMPVNQAQTYRAVPNMPQQRQDQHHQSAMMHPASAAGPPIAATP
PAYSTQYVAYSPPQQFPNQPLVQHVPHYQSQHPHVYSPVIQGNARMMAPPTHAQPGLV
SSATQYGAHEQTHAMYACPKLPYNKETSPSFYFAISTGSLAQYAHPNATLHPHTPHP
QPSATPTGQQSQHGGSHPAAPSPVQHQQHQAALHLASPQQQSAIYHAGLAPTPPSM
TPASNTQSPQNSFPAAQQTVFTIHPSHVQPAYTNPPHMAHVPQAHVQSGMVPSHPTAH
APMMLMTTQPPGGPQAALASALQPIPVSTTAHFPYMTHPVQAHHQQL"
BASE COUNT      1144 a    1380 c    1014 g    943 t
ORIGIN

```

```

Query Match          94.1%; Score 25.4; DB 9; Length 4481;
Best Local Similarity 96.3%; Pred. No. 62;
Matches 26; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

```

```

Qy      1 cgctcggcgcccgcgcgccccgcgc 27
          |||||
Db      539 CGCTCGGCGCCCGTGCCTCCCCGCCGC 565

```

SEQ ID NO: 1

RESULT 2

HSU70323

LOCUS HSU70323 4481 bp mRNA PRI 20-NOV-1996

DEFINITION Human ataxin-2 (SCA2) mRNA, complete cds.

ACCESSION U70323

VERSION U70323.1 GI:1679683

KEYWORDS .

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4481)

AUTHORS Pulst,S.-M., Nechiporuk,A., Nechiporuk,T., Gispert,S., Chen,X.-N.,
Lopes-Cendes,I., Pearlman,S., Starkman,S., Orozco-Diaz,G.,
Lunkes,A., DeJong,P., Rouleau,G.A., Auburger,G., Korenberg,J.R.,
Figuerola,C. and Sahba,S.

TITLE Moderate expansion of a normally biallelic trinucleotide repeat in
spinocerebellar ataxia type 2

JOURNAL Nature Genet. 14 (3), 269-276 (1996)

MEDLINE 97051920

REFERENCE 2 (bases 1 to 4481)

AUTHORS Pulst,S.-M.

TITLE Direct Submission

JOURNAL Submitted (10-SEP-1996) Medicine, Cedars-Sinai, 8700 Beverly Blvd.,
Los Angeles, CA 90048, USA

FEATURES Location/Qualifiers

source

1. .4481

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="12"

/map="12q24.1"

gene

163. .4101

/gene="SCA2"

CDS

163. .4101

/gene="SCA2"

/standard_name="spinocerebellar ataxia type 2"

/codon_start=1

/product="ataxin-2"

/protein_id="AAB19200.1"

/db_xref="GI:1679684"

/translation="MRSAAAAPRSPAVATESRRFAAARWPGWRSRQRPARRSGRGGGG
AAPGPYPSPAAPPPPGPGPPPSRQSSPPSASDCFGSNGNGGGAFRPGSRRLGLGGPPR
PFVVVLLPLASPGAPPAAPTRASPLGARASPPRSGVSLARPAPGCPRPACEPVYGPLT
MSLKPQQQQQQQQQQQQQQQQQQQQPPPAANVRKPGSGLLASPAAPSPSSSSV
SSSSATAPSSVVAATSGGGRPGLGRGRNSNKGLPQSTISFDGIYANMRMVHILTSVVG
SKCEVQVKNGGIYEGVFKTYSKCDLVLDAAHEKSTESSSGPKREEIMESILFKCSDF
VVVQFKDMDSSYAKRDAFTDSAISAKVNGEHKEKDLEPWDAGELTANEELEALENDVS
NGWDPNDMFRYNEENYGVVSTYDSSLSSYTVPLERDNSEEFKREARANQLAEIESS
AQYKARVALENDDRSEEEKYTAVQRNSSEREHGSINTRENKYIPPGQRNREVISWGS
RQNSPRMGQPGSGSMPSRSTSTSTSDFNPNSSGSDQRVVNGGVWPSPCPSPPSRPPSR
QSGPNSLPPRAATPTRPPSRPPSRPPSHPSAHGSPAPVSTMPKMSSEGPPRMSP
KAQRHPRNHRVSAGRGSISSGLEFVSHNPPSEAAATPPVARTSPSGGTWSSVSGVPR
SPKTHRPRSPRQNSIGNTPSGPVLASPAQAGIIPTEAVAMPIPAASPTPASPNRAVT
PSSEAKDSRLQDQRQNSPAGNKENIKPNETSPSFSKAENKGISPVVSEHRKQIDDLKK
FKNDFRLQPSSTSESMDQLLNKNREGEKSRDLIKDKIEPSAKDSFIENSSNCTSGSS
KPNSPSISPSILSNTEHKRGPEVTSQGVQTSSPACKQEKDDKEEKDAAEQVRKSTLN
PNAKEFNPRSFSPQPKPSTTPTSPRQAQPSPSMVGHQQPTPVYQPVCFAPNMMYPVP
VSPGVQPLYPIPMTPMPVNQAKTYRAVPNMPQQRQDQHHQSAMMHPASAAGPPIAATP
PAYSTQYVAYSPQQFPNQPLVQHVPHYQSQHPHYVSPVIQGNARMMAPTHAQPGLV
SSATQYGAHEQTHAMYACPKLPYNKETSPSFYFAISTGSLAQYAHNPATLHPHTPHP
QPSATPTGQQQSQHGGSHAPSPVQHHQHQAALHLASPPQQQSAIYHAGLAPTTPPSM

TPASNTQSPQNSFPAAQQTVFTIHPSHVQPAYTNPPHMAHVPQAHVQSGMVPSHPTAH
APMMLMTTQPPGGPQAALAQSAIQPIPVSTTAHFPYMTGPSVQAHHQQL"
BASE COUNT 1144 a 1380 c 1014 g 943 t
ORIGIN

Query Match 100.0%; Score 24; DB 9; Length 4481;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctccgcctcagactggttttggtag 24
|||
Db 375 CTCCGCCTCAGACTGTTTGGTAG 398

SEQ ID NO: 2

RESULT 4

HSU70323/c

LOCUS HSU70323 4481 bp mRNA PRI 20-NOV-1996

DEFINITION Human ataxin-2 (SCA2) mRNA, complete cds.

ACCESSION U70323

VERSION U70323.1 GI:1679683

KEYWORDS .

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4481)

AUTHORS Pulst,S.-M., Nechiporuk,A., Nechiporuk,T., Gispert,S., Chen,X.-N.,
Lopes-Cendes,I., Pearlman,S., Starkman,S., Orozco-Diaz,G.,
Lunkes,A., DeJong,P., Rouleau,G.A., Auburger,G., Korenberg,J.R.,
Figueroa,C. and Sahba,S.

TITLE Moderate expansion of a normally biallelic trinucleotide repeat in
spinocerebellar ataxia type 2

JOURNAL Nature Genet. 14 (3), 269-276 (1996)

MEDLINE 97051920

REFERENCE 2 (bases 1 to 4481)

AUTHORS Pulst,S.-M.

TITLE Direct Submission

JOURNAL Submitted (10-SEP-1996) Medicine, Cedars-Sinai, 8700 Beverly Blvd.,
Los Angeles, CA 90048, USA

FEATURES Location/Qualifiers

source

1. .4481
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
/map="12q24.1"

gene

163. .4101
/gene="SCA2"

CDS

163. .4101
/gene="SCA2"
/standard_name="spinocerebellar ataxia type 2"
/codon_start=1
/product="ataxin-2"
/protein_id="AAB19200.1"
/db_xref="GI:1679684"
/translation="MRSAAAAPRSPAVATESRRFAAARWPGWRSRQPARRSGRGGG
AAPGPYPYSAAPPPPGPGPPSRQSSPPSASDCFGSNGNGGGAFRPGSRRLGLGGPPR
PFVVVLLPLASPGAPPAAPTRASPLGARASPPRSGVSLARPAPGCPRPACPEVYGPLT
MSLKPQQQQQQQQQQQQQQQQQQQQPPPAANVRKPGGSGLLASPAAPSPSSSSV
SSSSATAPSSVVAATSGGGRPGLGRGRNSNKGLPQSTISFDGIYANMRMVHILTSVVG
SKCEVQVKNGGIYEGVFKTYSKCDLVLDAAHEKSTESSGPKREEIMESILFKCSDF
VVVQFKDMDSSYAKRDAFTDSAISAKVNGEHKEKDLEPWDAGELTANEELEALENDVS
NGWDPNDMFRYNEENYGVVSTYDSSLSSYTVPLERDNSEEFKREARANQLAEIESS
AQYKARVALENDDRSEEEKYTAVQRNSSEREHGSINTRENKYIPPGQRNREVISWGSG
RQNSPRMGQPGSGSMPSRSTSHTSDFNPNSGSDQRVVNGGVWPSPCPSRSSRPPSR
QSGPNSLPPRAATPTRPPSRPPSRPPSHPSAHGSPAPVSTMPKRMSSEGPPRMSP
KAQRHPRNRHVSAGRGSISSGLEFVSHNPPSEATPPVARTSPSGGTWSSVVGVPRL
SPKTHRPRSPRQNSIGNTPSGPVLASPAQAGIIPTEAVAMPIPAASPTPASPNRAVT
PSSEAKDSRLQDQRQNSPAGNKENIKPNETSPSFSKAENKGISPVVSEHRKQIDDLKK
FKNDFRLQPSSTSESDQLLNKNREGEKSRDLIKDKIEPSAKDSFIENSSSNTSGSS
KPNSPSISPSILSNTHEHKGPEVTSQGVQTSSPACKQEKDDKEEKDAAEQVRKSTLN
PNAKEFNPRSFSPKPTSTPTSPRPQAQPSPSMVGHQOPTPVYTPVCFAPNMMYPVP
VSPGVQPLYPIPMTPMPVNQAKTYRAVPNMPQQRQDQHHQSAMMHPASAAGPPIAATP
PAYSTQYVAYSPQQFPNQPLVQHVPYQSQHHPVYSPVIQGNARMAPPHTHAQPGLV
SSATQYGAHEQTHAMYACPKLPYNKETSPSFYFAISTGSLAQQYAHNPATLHPHTPH

QPSATPTGQQSQHGGSHAPSPVQHHQHQAALHLASPQQQSAIYHAGLAPTPPSM
TPASNTQSPQNSFPAAQQTFTIHPSHVQPAYTNPPHMAHVPQAHVQSGMVP SHPTAH
APMMLMTTQPPGGPQAALAQSALQPIPVSTTAHFPYMTHTPSVQAHHQQL"

BASE COUNT 1144 a 1380 c 1014 g 943 t
ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 4481;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtggccgaggacgaggagac 20
 |||||
Db 833 GTGGCCGAGGACGAGGAGAC 814